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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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5 ovis aries
5 cervus elap
2 gallus gall
5 columba liv
7 oryctolagus
2 mus musculu
4 gallus gall
6 sus scrofa
1 oryctolagus
2 meleagris g
4 columba liv
7 homo sapien
7 homo sapien
7 homo sapien
8 mus musculu
9 rattus norv
6 drosophila
1 mus musculu
1 macaca mula
1 homo sapien
2 rattus norv
5 caulobacter
3 mus musculu
6 rattus norv
6 drosophila
7 homo sapien
8 mus musculu
9 rattus norv
9 caulobacter
9 mus musculu
RESULT

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TALALORENT	HXKA_YEAST	CNTR_HUMAN	IL6A_PIG	DIM1_CAEEL	IL7R_MOUSE	CYRB_MOUSE	SUSY_PHAAU	EPA2_HUMAN	SUSY_SOYBN	IRA1_MOUSE	LIFR_HUMAN
Carara oreocurours		P26992 homo sapien	018796 sus scrofa	Q18066 caenorhabdi	P16872 mus musculu	P26955 mus musculu	Q01390 phaseolus a	P29317 homo sapien	P13708 glycine max	Q62406 mus musculu	

ALIGNMENTS

POR	HUMAN CONTROL DOOR
i n	77 77 77 77 77 77 77 77 77 77 77 77 77
	01-NOV-1990 (Rel. 16, Created)
	(Rel. 41,
	Erythropoietin receptor precursor (EPO-R). EPOR.
. Ω	sapiens (Human).
ភ ក	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
×	I_TaxID=9606;
Z	
ŧΰ	SEQUENCE FROM N.A.
≨ ∺	MEDLINE=91372359; PubMed=1654273; Ehrenman K., St John T.;
H3 :	e: cloning and
Ä	ple transcripts in an erythroid cell line OCIM1.";
žĤ	Exp. Hematol. 19:973-977(1991). [2]
Ť	UENCE FROM N.A.
> >	Jones S.S., D'Andrea A., Haines L.L., Wong G.G.;
Ä	clonin
ΗH	Blood 76:31-35(1990).
ž	[3]
ם ים	SEQUENCE FROM N.A. TISSUE=Placenta:
×	; PubMed=1668606;
	ae
	"Cloning of the human erythropoietin receptor gene.";
žΈ	556(1991).
ל ס	(4) SEQUENCE OF 1-96 FROM N.A.
ָה ה	TISSUE-Placenta;
×	92399734; PubMed=1668607;
	Chretien S.;
	"Cloning of the gene encoding the human erythropoietin receptor.";
žΡ	2557-2563(1991).
ב סי	SEQUENCE OF 1-17 FROM N.A.
×	MEDLINE=92147143; PubMed=1664413;
8 P	
7 14	"Genomic organization of the human erythropoletin receptor gene."; Genomics 11:974-986/1991)
zt	[6]
סי	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.
×	
> >	Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,
ij	"Functional mimicry of a protein hormone by a peptide agonist: the
T	2.8 A.";

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Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
Elliott S., Sitney K., Katz B.A., Matthews D.J., Wendoloski J.J.
Eggre J., Stroud R.M.;
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Livnah O., Johnson D.L., Stura E.A.,
                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (2.7
                                                     1 KFESKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e by non-profit institutions as long as its content is in no way dified and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BL; M34986; AAA52401.1;

BL; M60459; AAA52403.1;

BL; S45332; AAB23271.1;

BL; M76595; AAA52393.1;

BL; M77244; AAA52392.1;

BL; M77244; AAA52392.1;

BL; M43799; A43799.

BL; A43799; A43799.

BL; A43799; A43799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way that the structure of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST F
MECHANISM OF ERYTHROPOIETIN-INDUCED AND DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00060;
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                                                                                                          Similarity 93.8
98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
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18-NOV-98.
01-OCT-99.
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                                                                                                             Score 1060; DB 1;
Pred. No. 5.7e-96;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR POTENTIAL. CYTOPLASMIC (PFIBRONECTIN TY
                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (P
F9F326E162E9512A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERYTHROPOIETIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Farrell F.X., Bar
W., Krause C.D.,
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                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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                                                                                                                                                                         Length
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SEQUENCE
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TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q07303;
01-FEB-1995
                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                       InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND DIFFERENTIATION.

-:- SUBSELULLAR LOCATION: Type I membrane protein.

-:- SIMILARITY: BELLONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-:- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995
01-FEB-1995
                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                               PIR; A46713; i
HSSP; P19235;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D13566; BAA02761.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characteristics. Comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tabira
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93266574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                       Pfam; PF00041; fn3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional erythropoietin receptor of the cells with neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3iol. Chem. 268:11208-11216(1993).
FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
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T., Sasaki R.;
                                                                                                                                                                                                                                                                                 SM00060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chem.
                                                                                                                                                                                                                                                         PS01352; HEMATOPO_REC_L_F1;
                                                                                                                                                                                                                                    Transmembrane;
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                                                                                                                                                                                                                                                                                 FN3;
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M., Takahata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31, Created)31, Last sequence update)31, Last annotation updat
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    MW.
                                        POTENTIAL.
CYTOPLASMIC
FIBRONECTIN '
BY SIMILARIT'
BY SIMILARIT'
                          N-LINKED
                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                    BY SIMILARITY.
ERYTHROPOIETIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
    AC79AF22D06A7312 CRC64;
                                             SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor
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                            (GLCNAC.
                                                                                                                                                                                                                                  Signal.
                                                                                               TYPE-III.
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                       .) (POTENTIAL).
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RESULT 3
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE=Liver;
MEDLINE=91080149; PubMed=2175360;
Kuramochi S., Ikawa Y., Todokoro K.;
"Characterization of murine erythropoietin"
J. Mol. Biol. 216:567-575(1990).
                                                                                                                                                                                                                                                                                                                                                                                        D'Andrea A.D., Lodish H.F., Wong G.G.; "Expression cloning of the murine erythropoletin Cell 57:277-285(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Mus musculus (Mouse).
'~rvota; Metazoa; Chordata;
'~rvota; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                       "Spleen focus-forming virus long terminal repeat activation of the murine erythropoietin receptor friend leukemia cell line.";
                                                                                                              MEDLINE=91201346; PubMed=1849897; Lacombe C., Chretien S., Lemarcha Gisselbrecht S., Cartron J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=92017832; PubMed=1656233;
Hino M., Tojo A., Misawa Y., Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89195238; PubMed=2539263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythropoietin
                                                                                                                                                                                   SEQUENCE OF 1-24 FROM N.A.
                                                                                                                                                                                                                                                                                               Youssoufian
                                                                                                                                                                                                                                                                                                               MEDLINE=90287158; PubMed=2162479;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-27 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                           Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRITIAVRARMAEPSFGGFWSAWSEPVSLLT
                                                                                                                                                                                                                            Cell. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYTFAVRARMAEPSFSGFWSAWSEPASLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTECVLSNLRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLADESGHVVIRWLPPPETPMTSHIRFELDISAGNGAGSVQRVELLEGRTECVLSNLRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HQAPTVRGSMRFWCSLPTADTSSFVPLELQVTEASGSPRYHRIIHINEVVLLDAPAGLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                                               Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                   transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor precursor (EPO-R)
                         266:6952-6956(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                          10:3675-3682(1990).
                                                                                                                                                                                                                                                                                                                                                                                  11:5527-5533(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.9%;
78.2%;
                                                                                                                                   Lemarchandel V.,
                                                                                                                                                                                                                                                                   Orkin S.H., D'Andrea A.D., Lodion of the mouse erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 877.5; DB 1;
Pred. No. 3.8e-78;
3; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                   Mayeux P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
                                                                    gene
                                                                                           insertional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes.";
                                                                                                                                     Romeo P.H.
                                                                                                                                                                                                                                                                                        Lodish
                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507;
                                                                    the T3C1-2
                                                                                                                                                                                                                                                                                        H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152
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Best Local S
Matches 164
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EMBL; X53081; CAA37248.1; -.
EMBL; M38133; AAA37572.1; -.
EMBL; M38133; AAA37582.1; -.
EMBL; S59388; AAA37582.2; -.
PIR; A32385; A32385.
PIR; A32385; A32385.
PIR; A41686; A41686.
PIR; S144081; S144081.
HSSP, P19235; 1EBA.
                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
DOMAIN
DISULFID
DISULFID
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miura O., Cleveland J.L., Ihle J.N.;
"Inactivation of erythropoietin receptor function in a region having homology with other cytokine remote the most cell. Biol. 13:1788-1795(1993).
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93180826; PubMed=8382775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - FUNCTION:
                         181
                                                     153
                                                                               121
                                                                                                          93
                                                                                                                                   61
                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS I FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERA AND DIFFERENTIATION.
                                                                                                                                                             KTESKAALLASRGSEELLCFTQRLEDLVCFWEEAASSGM-DFNYSFSYQLEGESRKSCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:95408; Epor.
                                                                                                                                                                            KFESKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRL
               TRITIAVRARMAEPSFGGFWSAWSEPVSLLT
                                                                     RLADESGHVVIRWLPPPETPMTSHIRFELDISAGNGAGSVQRVELLEGRTECVLSNLRGR
                                                                                                                        HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVA
TRYTFAVRARMAEPSFSGFWSAWSEPASLLT
                                                     RRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTECVLSNLRGG
                                                                                                          HQAPTVRGSVRFWCSLPTADTSSFVPLELQVTEASGSPRYHRIIHINEVVLLDAPAGLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00060; FN3; 1
E; PS01777
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                             25
25
250
273
273
147
52
90
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEMATOPO_REC_L_F1;
                                                                                                                                                                                                                                                                                   291
55194
                                                                                                                                                                                                                                                                                                             507
249
272
507
212
62
106
                                                                                                                                                                                                                              79.2%;
77.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hematopo_receptor_L_F1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                    WW;
                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL
FIBRONECTIN TYPE-III.
BY SIMILARITY.
N-LINKED (GLCNAC...)
E -> D (IN REF. 3; AAB
E -> D (57A2E26451CA CRC
                                                                                                                                                                                                                Score 869.5;
Pred. No. 2.3e
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                            ERYTHROPOIETIN RECEPTOR
                          211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal
                                                                                                                                                                                                                              .3e-77;
                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                            DВ
                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                  AAB20029).
                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptors.";
                                                                                                                                                                                                                                                                                                               .) (POTENTIAL).
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by point
                                                                                                                                                                                                                                              507;
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                                                                                                                                                                                                                   1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration - Loutstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            commercia.
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RESULT 4
                                                        Query Match
Best Local Similarity
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Q08351;
Q1-FEB-1995
Q1-FEB-1995
16-OCT-2001
                                                     DOMAIN
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPL OR TH
                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93390934; PubMed-8397366; Vigon I., Florindo C., Flichelson S., Guenet J.-L., Mattei Souyri M., Cosman D., Gisselbrecht S.; "Characterization of the murine Mpl proto-oncogene, a memb hematopoietic cytokine receptor family: molecular cloning, chromosomal location and evidence for a function in cell goncogene 8:2607-2615(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             superfamily that transduces EMBO J. 12:2645-2653(1993).
                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skoda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=93327753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor precursor
                                                                                                                                            DOMAIN
                                                                                                                                                      CHAIN
                                                                                                                                                                             Receptor;
                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                               Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                         InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1
                                                                                                                                                                                                                                               MGD; MGI:97076; Mpl.
InterPro; IPR002996;
                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ICFW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine c-mpl: a member of the hematopoietic growth factor receptor
                                                                                                                                                                                                                                                                       BL; Z22649; CAA80365.1;
BL; Z22657; CAA80372.1;
BL; X73677; CAA52031.1;
R; S35317; S35317;
SP; P19235; 1EBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A I MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES. SUBCELLULAR LOCATION: Type I membrane protein. SUBCELLULAR LOCATION: Type I TOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR TPOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.C.,
                                                                                                                                                                                                   SM00060; FN3;
                                                                                                                                                                                         PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (C-mpl).
                                                                                                                                                                             Transmembrane;
                                                                             26
26
28
483
505
117
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 31, Created)
(Rel. 31, Last sequence u
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seldin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transduces a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8334987;
n D.C., Chiang M
                                                                                                                                                                         HEMATOPO_REC_L_F1; 1.
mbrane; Glycoprotein; Signal; Repeat
                                                                             625
482
504
625
117
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                        69817
        15
24
        . 63
                                                        M.
                                                                                    POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (P.

(TINKED (TINKEF. 2).
       Score 171;
Pred. No. 4
                                                                                                                                        THROMBOPOIETIN RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferative signal.";
                                                       -> PVRTSPAGE (IN 309CF6EAA3724549
                                                                             -> V (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tion update)
(TPO-R) (Myeloproliferative leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625
                                                                                                                                                                                                                                                                                                                                                         moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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01-FEB-1995
16-OCT-2001
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                       This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=94292186; PubMed=8020956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and transcription of
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                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMURE RESPONSES.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; C-MPL-K (SHOWN HERE) AND C-MPL-P; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED AT A LOW LEVEL IN A LARGE NUMBER OF CELLS OF HEMATOPOLETIC ORIGIN. THE TWO FORMS (C-MPL-K AND C-MPL-P) ARE ALWAYS FOUND TO BE COEXPRESSED.

DISBASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGARARYOCYTIC THOMOSOMEOUTH A LARGE A CAUSE OF CONGENITAL AMEGARARYOCYTIC COMPONENCY OF COMPLANCE OF CONGENITAL AMEGARARYOCYTIC THOMOSOMEOUTH A CAUSE OF CONGENITAL AMEGARARYOCYTIC COMPONENCY OF COMPLANCE OF CONGENITAL AMEGARARYOCYTIC COMPONENCY OF COMPANY.
                                                        SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-8 IS THE INIT! DATABASE: NAME-PROW; NOTE-CD guide CD110 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/11586825_g.htm"
                                                                                                                                                           SIMILARITY:
                                                                                                                                                                                                        THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED THROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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.; M90103; AAA69972.1;
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.; U68159; AAB08424.1;
.; U68160; AAB08424.1;
.; U68161; AAB08424.1; J
                                      MAEPSFGGFWSAWSEPVSL 209
                                                                                                                                                                                                   LADESGHVVIRW-LPPPETPMTSHIRFEL----DISAGNGAGSVQRVE
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IPR003528;
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Hematopo_receptor_L_F1.
278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

RIKHALMPSLPDLHRVLGQYLBDTAALSPKATVSDTCEEV

EPSLLEILPKSSERTP -> YRDRQAGDWRWTRWSRTCKQA

FLVRSYTPDLREPPVRTYGFALPARHLMDSPRLLTL (IN
                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 146;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ISOFORM C-MPL-P).
A -> V (IN DBSNP:6087).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOFORM C-MPL-P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_011988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_011989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> K (IN DBSNP:6088).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D25D8D8959359DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                       -LLEGRTECVLSNLRGRTRITIAVRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                  .4e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                               107;
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no
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PRESULT 6

PRILR_BOVIN

ID

PRILR_BOVIN

AC

208172;

D7

O1.NOV-1997 (Rel. 35, Created)

D7

O1.NOV-1997 (Rel. 35, Last sequence update)

D7

O1.NOV-1997 (Rel. 36, Last annotation update)

D7

O1.NOV-1997 (Rel. 36, Last annotation update)

D7

O1.NOV-1997 (Rel. 36, Last annotation update)

D8

D9

PRILR.

OS

Bos taurus (Bovine)

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebra;

OC

Mammalia; Eutheria; Cetartiodactyla; Ruminantia;

OC

Bovidae; Bovinae; Bos.

OR

ROMANNALIA SSUBLE-Endometrium;

RX

MEDLINE=92246019; PubMed=1338725;

RN

[1]

RP

SCOUTT P., Kessler M.A., Schuler L.A.;

"Molecular cloning of the bovine prolactin receptor utaro-placental tissues.";

Of prolacental rissues.";

RX

MOL Cell. Endocrinol. 89:47-58(1392).

CC

-1-SUBCLELLUAR LOCATION: Type I membrane proteince in the composition of the cytoxine Family of of Type-II

FINE Family of the Cytoxine Family of the Cytoxine Family of the Cytoxine Fami
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of the bovine prolactin receptor and
of prolactin and growth hormone receptor transcripts in
  75
                                                                                                             20
                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                   APTARGAIRFWCSLPTADTSSFVPLELRLTA-----ASGAPRFHRVIHINEVVLLDAPV 116
                                                                                                                                                           ALLAARGPEE----LLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQ
CPDYKTGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLY---VHVTYIVEPEPPA
                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ender the second of the anterior pituitary hormone on: This is a receptor for the anterior pituitary hormone
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                 10.7%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Signal; Repeat.
POTENTIAL.
                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIA)
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                    Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                 Score 118; DB 1;
Pred. No. 0.00068;
                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
; 7385C0D6956EE139 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROLACTIN RECEPTOR
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                                                                                                                                                                                                                          101;
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                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                          Length 581
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                                                                                                                                                                                                                       Indels
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GHR_BOULT
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Best Local
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01-NOV-1997 (Re
01-NOV-1997 (Re
Growth hormone
                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                             CARBOHYD
CARBOHYD
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CARBOHYD
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X70041; CAA49635.1;
HSSP; P10912; 1HWH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
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           35;
                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
           Conservative
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157
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nbrane; Glycoprotein; Signal.
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260
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248
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                                    10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
or precursor (GH recep
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                                                                                                                                              ¥.
                                                                                                                                   POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC...) (PO
N-LINKED (GL
             25;
     Score 112.5;
Pred. No. 0.00
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GROWTH HORMONE RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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. 0.0026;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor) (Serum
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                                                                                                                                              CRC64;
                                                             Length
             Indels
                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROWTH HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding
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                                                                634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovoidea;
           13;
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                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interlaukin-9 receptor precursor (IL-9R).
(IL9RX OR IL9R) AND (IL9RY OR IL9R).
                 EMBL;
EMBL;
EMBL;
                                                                  use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-94250901; PubMed-8193355;
Chang M.S., Engel G., Benedict C.,
"Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                    Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                          gene.
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MEDLINE=92302307; PubMed=1376929;
Renauld J.C., Druez C., Kermouni
van Roost E., van Snick J.;
                                                                                                                                                                                                                                                                                            SEQUENCE
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                 , M84747; AAA58679.1;
, S71404; AAB30844.2;
, S71420; AAD14081.1;
, L39064; AAC29513.1;
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ikora J.P., Higgs D.R.,
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Matches 53
                                                                                                                    GHR_SHEEP STANDARD; PRT; 634 AA. 0.20575; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation updat
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Mammalia; Eutheria; Cetartiod
Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
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                           European Bioinformatics Institute.
                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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IPR003531; Hematopo_receptor_S_F1.
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Kelly P.A., Jabbour H.N.;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9860;
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evidence for
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Best Local
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                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
Growth hormone receptor precursor (GH recep
                                                                                                                                                                                               protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X94953; CAA64419.1;
HSSP; P14787; LAN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
NCBI_TaxID=9031;
                                                              Archosauria; Aves;
                                                                                                  Eukaryota;
                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 RITIAVRARMAEPSFGGFWSAWSEPVSL 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 PEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAPTARGAIRFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROLACTIN.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
SIMILARITY: CONTAINS 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYFSKKHTSIWKIYVITVNAINQMGVSSSDPLY---VDVTYIVEPEPPANLTLELKHPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSLPTADTSSFVPLELRLTA-----ASGAPREHRVIHINEVVLLDAPVGLVARL---AD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKPYLWIKWFPPTLTDVKSGWFMIQYEIRLKPETAAD--WEIHFAAKQTQLKIFSLYPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESGHVVIRWLPPPETPMTS----HIRFELDISAGNGAGSVQRVELLEGRTECVLSNLRGRT
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l Similarity 20.7%;
43; Conservative '
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IPR003961; FN_III.
IPR003528; Hematop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                  Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    581 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMATOPO_REC_L_F1;
                                                           Neognathae;
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                                                                                            Chordata;
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BY SIMILARITY.
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THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
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CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

BY SIMILARITY.

BY SIM
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Pred. No. 0.0064;
1; Mismatches 9
                                                           Craniata; Vertebrata; Euteleostom1;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
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receptor)
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                                                                                                                                                                                                                         (Serum
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(POTENTIAL).
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Best Local :
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CARBOHYD
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Burnside J., Liou S.S., Cogburn L.A.;
Molecular cloning of the chicken growth hormone receptor
complementary deoxyribonucleic acid: mutation of the gene
sex-linked dwarf chickens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M74057; AAA48781.1; -. PIR; S32823; S32823. HSSP; P10912; 1HWH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: BROAD SPECIFICITY.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENDOCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
                          179
                                                   137
                                                                            127
193 MGRDYEIRVRSRQRTSEKFGEF
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                                                                                                                              69
                                                                                                                                                     29
                                                                                                                                                                             14 PEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQL-----EDEPWKLCRLHQAPTARG
                                                                                                                                                                                                                   Local Similarity
                                                   GIHGDIQVRWDPPPTADVQKGWITLEYELQYKEVNET---
                        GRTRITIAVRARM-AEPSFGGF
                                                                            ---GHVVIRWLPPPETPMTS---HIRFELDISAGNGAGSVQRVELLEGRTECV--LSNLR
                                                                                                   AGENSCYFNTSYTSIWIPYCVKL-ANKDEVFDEKCFSVDEIVLPDPPVHLNWTLLNTSQT
                                                                                                                              AIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVARLADES--
                                                                                                                                                       PQISKCRSPELETFSCYWTD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                     809
                                                                                                                                                                                                                                                                                    238
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26.7%;
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                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                       26;
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                          199
                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                   Score 107;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC FIBRONECTIN
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                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
TYPE-III.
                                                                                                                                                                                                                   .0085;
                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                      90;
                                                    -KWKELEPRLSTVVPLYSLK 192
                                                                                                                                                                                                                               Length 608
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) (POTENTIAL).
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RESULT 12 GHR_COLLI

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Best Local S
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                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
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01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR0039528; Hematopo_receptor_L_F1.
InterPro; IPR003528; Hematopo_receptor_L_F1.
SMART; SM00061; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (si or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on in
                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified
                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U20353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHR_COLLI
                                                                                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P10912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Columba livia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISSUE=Liver;
                     127
                                                                                                  12
                                        82
                                                           70
                                                                              27
                                                                                         RGPEELLCETERLEDLVCFFEEAASAGV-GPGNFSFSF-QLEDEPWKLCRLHQAPTARGA
GIHGDIQVRWDPPPTADVQKGWITLEYELQYKEVNET----
                                                 IRFWCSLPTADTSSFVPLELRLTAASGAPRF-HRVIHINEVVLLDAPVGLVARLADES---
                                                                            RLPQISKCRSPELETFSCYWTDGNFYNLSAPGTIQLLYMKRNDEDWKEC-----PDYITA
                                      GENSCYFNTSYTSIWIPYCVKLVNKDEV--FDEKCFSVDEIVLPDPPVHLNWTLLNTSQT
                                                                                                                      53;
                                                                                                                   Similarity 26.:
53; Conservative
                 -GHVVIRWLPPPETPMTS---HIRFELDISAGNGAGSVQRVELLEGR--TECVLSNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                Transmembrane;
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21
241
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265
119
34
75
100
16
53
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89
130
135
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(Rel. 35, Last sequence up)
(Rel. 35, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neognathae;
                                                                                                                                                                                       53
130
135
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                                                                                                                           9.5%;
26.2%;
                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal.
                                                                                                                                                                      MW;
                                                                                                                     28;
                                                                                                                                                                            CYTOPLASMIC (PO)
FIBROMECTIN TYP)
BY SIMILARITY.
BY SIMILARITY
N-LINKED (GLCNA)
                                                                                                                  Score 104.5;
Pred. No. 0.01
8; Mismatches
                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                           GROWTH HORMONE RECEPTOR.
                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
; Columbiformes; Columbidae; Columba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                    C48750BF9EE4EBDA CRC64;
                                                                                                                            104.5; DB
No. 0.015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                     TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                    96;
                                                                                                                                      1;
 KWKELEPRLSTMVPLYSLK
                                                                                                                                                                                     .) (POTENTIAL).
                                                                                                                                      Length
                                                                                                                    Indels
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(POTENTIAL).
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MBL outstation -
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PRLR_RABIT
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Proc No. 1
                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00041; fn3; SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no use by non-profit institutions as long as its con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins 27:459-468(1997).
-!- FUNCTION: THIS IS A RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97248733; PubMed=9094747;
Halaby D., Thoreau E., Djiane J., Morno
"Homology modeling of rabbit prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P14787;
01-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRLR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRLR_RABIT
                                                                                                                                                                                                                                                                                                                                                               Receptor;
                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1AN3; 03-DEC-97.
rPro; IPR002996; CR1A.
rPro; IPR003961; FN_III.
rPro; IPR003528; Hemator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A30304; A30304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGRDYEIRVRSRQRTSEKFGEF
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                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
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124
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                                                                                                                                                                                                                                                                                                                                                                                            HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A.
                          616
234
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  68840
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                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Sig
BY SIMILARITY
  ¥.
                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIA)
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
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                          N-LINKED
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                                                                                                                                                                                                                                                                                                          PROLACTIN RECEPTOR
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  800E3166FEF7108C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mornon J.P.; actin hormone
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                       GLCNAC. .
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                             (POTENTIAL)
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Matches
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Growth hormone receptor precursor (GH
                                  Receptor
                                                                          "An exon carboxy t
REVISIONS.
STRAIN-C57BL;
                                                                                                                                                                                                                                                                                                                                                                                                                             "Mouse serum growth hormone (GH) binding proextracellular and substituted transmembrane Mol. Endocrinol. 3:984-990(1989).
                                                                                                                                                  SEQUENCE OF 156-650
                                                                                                                                                                                                                                                     STRAIN=Swiss Webster, MEDLINE=95080157; Pub
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Swiss Webster, and DBA/2J; MEDLINE=99367316; PubMed=10425445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AN MEDLINE=89295449; PubMed=2739661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                      MEDLINE=95201642;
                                                                                                                                                                                             splicing.";
                                                                                                                                                                                                          receptor transcripts
                                                                                                                                                                                                                                      Edens A., Southard J.N., Talamantes F.;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                         Moffat J.G., Edens A.,
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                              hormone
                                                                                                                                                                              Endocrinology 135:2802-2805(1994)
                                                                                                                                                                                                                                                                                                                            hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GHBP)
                                                                                                                                                                                                                          Mouse
                                                                                                                                                                                                                                                                                                                                          "Structure and expression of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILSLYPGQKYLVQVRCK---PDH-GFWSVWSPESSI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLEVKHPEDRKPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAA--EWETHFAGQQTQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VARLADESGHVVIRWLPPPETPMTS---HIRFELDISAGNGAGSVQRVELLEGRTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYKTGGPNSCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRY---VDVTYIVEPDPPVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TARGAIRFWCSLPTADTSSFVPLELRLTAAS-----GAPRFHRVIHINEVVLLDAPVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPFIFKCRSPEK-----ETFTCWWRPGADGGL-PTNYTLTYHKEGE----TITHECP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLSNLRGRTRITIAVRARMAEPSFGGFWSAWSEPVSL
                                                                                                                                                                                                                       growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Serum binding
                                              receptor gene.";
r 4:223-227(1994)
                                                                          n encoding the mouse terminus is located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                             binding protein gene.";
Endocrinol. 23:33-44(1999).
                                                                                         encoding
                                                                                                      He L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuniyoshi J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
                                                                                                                                                                                                         hormone receptor/binding scripts are produced from
                                                                                                        Kopchick J.J
                                                                                                                                                                                                                                                     ter, and DBA/2J;
PubMed=7988474;
                                                                                                                      PubMed=7894338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORMS 1 AND
                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein).
                                                                                                                                                                                                                                                                                                                                                         Talamantes F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Talamantes F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                          growth hormone between exon 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                 (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
receptor)
                                                                                                                                                                                                          protein a
a single
                                                                                                                                                                                                                                                                                                                                          growth hormone receptor/growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                          binding protein (mGHBP) and 8 of the mouse grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1:
                                                                                                                                                                                                                                                                                                                                                                                                                                              domains.";
                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 616;
                                                                                                                                                                                                       and growth hormone gene by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein)
                                                                          growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
      CARBOHYD
CARBOHYD
                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                          Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWI
between
                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                           CARBOHYD
                                                                                                                                                 DOMAIN
                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
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                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                      PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 25-41 MEDLINE-88288223;
                                                                                                                                     DOMAIN
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hormone receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AF120481;
AF120482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF120488;
AF120487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF120485;
AF120486;
AF120487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF120483;
AF120484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF120481;
AF120482;
                                                                                                                                                                                                                                                                                                                                                                                      AF120486;
                                                                                                                                                                                                                                                                                                                                                                                                                                AF120483;
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274
274
298
298
153
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271
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EMBL; U49266; AAK62802.1; EMBL; U49268; AAK62802.1; EMBL; U49268 AAK62802.1; EMBL; U493933; AAK62802.1; HSSP; P10912; 1HWH. MGD; MGI:95708; Ghr.
                                                                                                                                                                                                                                                                 InterPro; IPR002996; (InterPro; IPR003961; InterPro; IPR003528; InterPro; IPR003528; InterPro; IPR0041; In3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith W.C., Colosi P., Talamantes F.; "Isolation of two molecular weight variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou Y., He L., Kopchick J.J.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECTETED (1SOFORM 2).

ALTERNATIVE PRODUCTS: 2 isoforms; 1/HMW GHR (shown here)
GHR; are produced by alternative splicing.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           concentration of gh. SUBUNIT: ISOform 1 is SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Isoform 1 is a recept hormone. Isoform 2 is a serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             may play an important role in regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss institute of Bioinformatics and the EMBL outstation resuropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M33324; AAA37690.1;
M31680; AAA37689.1;
AF120489; AAD32556.
                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD32556.1;
AAD32555.1;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAD32555
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AAD32556.1;
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AAD32556.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD32555
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                                                                                                                                                                                                                                                   HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=3398846;
24
650
273
297
650
260
260
120
123
1164
1164
208
                                                                                                                                                                                                                                                                                   Hematopo_receptor_L_F1
                                                                                                                                                                                                                                                                                                    FN_III.
                                                                                                                                                                                                                                  Glycoprotein; Signal; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                      JOINED.
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                                                                                                                                POTENTIAL.
CYTOPLASMIC
FIBRONECTIN
                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor for
                                                                                                                                                                                                    GROWTH HORMONE RECEPTOR
                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ptor for pituitary gland growth hormone binding p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                  TYPE-III.
                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth
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N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
DIQFPWFLIIIFGIFGVAVMLFVVIF -> GTKSNSQHPHQ
EIDNHLYHQLQRIRH (IN ISOFORM 2).

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PRESULT PRESUL
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Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-WHITE LEGHORN; TISSUE-Kidney;

MEDLINE-93075121; PubMed-1445292;

Tanaka M., Maeda K., Okubo T., Nakashima K.;

Tanaka M., Maeda K., Okubo T., Nakashima K.;

"Double antenna structure of chicken prolactin receptor "Double antenna structure of chicken prolactin receptor the cDNA sequence."

"Double antenna structure of chicken prolactin receptor "Double antenna structure" "Double antenna structure of chicken prolactin receptor "Double antenna structure" "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIR_CHICK STANDARD; PRT; 831 AA Q04594; O1-JUN-1994 (Rel. 29, Created) O1-JUN-1994 (Rel. 29, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation updat 15-JUL-1998 (Rel. 36, Last annotation updat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWI
between
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CONFLICT
CONFLICT
                                  PIR; JQ1655; JQ1655.

HSSP; P14787; 1AN3.

InterPro; IPR002996; CRIA.

InterPro; IPR003961; FN_III.

InterPro; IPR003528; Hematopo_receptor_L_F1.

Pfam; PF00041; fn3; 4.
                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROLACTIN.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 188:490-496(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prolactin receptor
                                                                                                                                                                                                                                            EMBL; D13154; BAA02439.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 GPIWLTYCPVYSLRMDKEHEVRVRSR--QRSFEKY-SEFSEVLRVI 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTLLNISLTGIRGDIQVSWQPPPNADVLKGWIILEYEI------QYKEVNESKWKVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRFTKCRSPELETFSCYWTEGDNPDLKTPGSIQLYYAKRESQRQAARIAHEWTQEWKEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARLADES -----GHVVIRWLPPPETP-MTSHIRFELDISAGNGAGSVQRVELLEGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PDYVSAGKNSCYFNSSYTSIWIPYCIKLT-TNGDLLDQKCFTVDEIVQPDPPIGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLV
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T -> A (IN REF. 3).
G -> A (IN REF. 3 AND 4).
E -> G (IN REF. 2).
R -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 103.5; D
Pred. No. 0.02;
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G -> A (IN REF. 3 AND 4).
E -> G (IN REF. 2).
R -> A (IN REF. 2).
95653380CAF0B931 CRC64;
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(CPRLP).
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                                                                                                                                                                                                                                                                                                                                                                                      There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01352;
 397
                                     337
                                                                                                                233
                                                                         280 DYRTAGPNSCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHY----VDVTYIVQPDPPVNV
                                                                                             65
                                                                                                                                 5 KAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAP
                                                                                            TARGAIRFWCSLPTADTSSFVPLELRLTAA-----SGAPRFHRVIHINEVVLLDAPVGL
FSLNPGKKYIIQIHCK - - - PDHHGSWSEWS
                  SNLRGRTRITIAVRARMAEPSFGGFWSAWS
                                    TLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQQTQYKM
                                                      VARL----ADESGHVVIRWLPPPETPMTS-HIRFELDISAGNGAGSVQRVELLEGRTECVL
                                                                                                              KPTIIKCRSPEK-----ETFTCWWKPGLDGG-HPTNYTLLYSKEGEE----QVYECP
                                                                                                                                                     42;
                                                                                                                                                                                                                     228
326
36
75
79
100
112
113
262
303
315
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               HEMATOPO_REC_L_F1;
                                                                                                                                                                                                             9.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Signal; Repeat
                                                                                                                                                                                                   MW;
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                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC...) (
                                                                                                                                                    Score 103.5;
Pred. No. 0.02
37; Mismatches
                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC
FIBRONECTIN
                                                                                                                                                                                                                                                                                                                 FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                   PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                  204
423
                                                                                                                                                             ; DB
                                                                                                                                                                                                                                                                                                                                               TYPE-III
                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                    102;
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                                                                                                                                                   Gaps
                                     396
                                                       174
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Search completed: August 28, 2002, 17:40:42 Job time: 533 sec